

Pred. No.: 1.3e-47 Length: 666
 Score: 515.50 Matches: 92
 Percent Similarity: 83.19% Conservative: 7
 Best Local Similarity: 77.31% Mismatches: 9
 Query Match: 83.69% Indels: 11
 DB: 8 Gaps: 2

US-09-541-462B-2 (1-108) x AY072430 (1-666)

Qy	1 MetAlaAlaAlaMetAspValAspThr-----ProSerGly----- 12
	::: :: :::
Db	85 TTAATGGCGACTCTAGACTCCGACGTTACCATGATTCCCTGCCGAGAACCTCCAGCAGC 144
Qy	13 -----ThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAla 29
	: : : : : : :
Db	145 GTAGCCGCCTCGTCTTCCAACAAGAAAGCTAACAGCTAAGCATTGCAAATTAGAAGTGAGCGCC 204
Qy	30 ValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIle 49
	: : : : : :
Db	205 GTTGCTCTCTGGGCTTGGGATATCGTTGACAACGTGCGATCTGCAGAAACCACATC 264
Qy	50 MetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThr 69
	: : : : :
Db	265 ATGGATCTTGTATCGACTGTCAGGCTAACAGGCCAGTGCACACTGAGATGGCACT 324
Qy	70 ValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLys 89
	: : : : : :
Db	325 GTAGCTGGGGGTTTGAATCACGCCCTCACTTCACTGCATCAGCAGATGGCTAAAG 384
Qy	90 ThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
	: : : : : :
Db	385 ACTCGTCAAGTTGTCCATTGGATAACAGTGAGTGGAGTTTCAGAAATATGGTCAC 441

RESULT 15

AY052401 357 bp mRNA linear PLN 16-OCT-2001
DEFINITION *Arabidopsis thaliana* ring box-1-like protein mRNA, complete cds.
ACCESSION AY052401
VERSION AY052401.1 GI:16186264
KEYWORDS
SOURCE *Arabidopsis thaliana*.
ORGANISM *Arabidopsis thaliana*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicots; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 357)
AUTHORS Okresz, L...
TITLE Direct Submission
JOURNAL Submitted (25-AUG-2001) Institute of Plant Biology, Biological Research Center, Temesvari krt. 62, Szeged H-6701, Hungary
FEATURES Location/Qualifiers
source 1. .357
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
CDS 1. .357
 /note="RBX1-2"
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/product="ring box-1-like protein"
/protein_id="AAL13435.1"
/db_xref="GI:16186265"
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BASE COUNT 91 a 83 c 94 g 89 t
ORIGIN

Alignment Scores:

Pred. No.:	8.67e-48	Length:	357
Score:	514.50	Matches:	92
Percent Similarity:	83.76%	Conservative:	6
Best Local Similarity:	78.63%	Mismatches:	8
Query Match:	83.52%	Indels:	11
DR:	8	Gaps:	2

US-09-541-462B-2 (1-108) x AY052401 (1-357)

Qy	3	AlaAlaMetAspValAspThr-----ProSerGly-----	12
	:::		:
Db	4	GCGACTCTAGACTCCGACGTTACCATGATTCCCTGCCGAGAACGCTCCAGCAGCGTAGCC	63
Qy	13	---ThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAla	31
:::::	: : : :		
Db	64	GCGTCGTCTTCCAACAAGAAAGCTAACGCGATTGCAAATTAAAGAAGTGGAGCGCCGTTGCT	123
Qy	32	LeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAsp	51
Db	124	CTCTGGGCTTGGGATATCGTTGTTGACAACCTGTGCATCTGCAGAAACACATCATGGAT	183
Qy	52	LeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla	71
Db	184	CTTTGTATCGAGTGTCAAGCTAACAGGCCAGTGCCACAAGTGAAGAGTGCACTGTAGCT	243
Qy	72	TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArg	91
Db	244	TGGGGGGTTTGCATCACGCCCTCCACTTCACTGCATCAGCAGATGGCTAAAGACTCGT	303
Qy	92	GlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis	108
Db	304	CAAGTTTGTCCATTGGATAACAGTGAGTGGAGTTTCAGAAATATGGTCAC	354

Search completed: April 4, 2003, 17:52:09
Job time : 1471 secs

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 4, 2003, 16:34:12 ; Search time 219 Seconds
(without alignments)
1110.575 Million cell updates/sec

A ROC1

ATGGCGGCAGCGATGGATGTGGATACCCGAGCGCACCAACAGCGGCCGGCAAGAAGCGCTTGAACTGAAAGTGGAAATGCAGTA 90
M A A A M D V D T P S G T N S G A G K K R F B V K K W N A V 30
GCCCTCTGGGCTGGGATAATTGTGGTTGATAACTGTGCCATCTGCAGGAACCACATTATGGATCTTGACATAGAATGTCAGCTAACAG 180
A L W A W D I V V D N C A I C R N H I M D L C I E C Q A N Q 60
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A S A T S B E C T V A W G V C N H A F H F H C I S R W L K T 90
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R Q V C P L D N R E W E F Q K Y G H * 108

B ROC2

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M F S L K K W N P V A M W S W D V E C D T C A I C R V Q V M 30
GATGCGCTGCTTAGATGTCAGCTGAAACAAACAAGAGGACTGTGGTGTGGCTGGGAGAATGTAATCATTCCCTCCACAACACTGCTG 180
D A C L R C Q A E N K Q E D C V V V W G E C N H S F H N C C 60
ATGTCCTGTGGGTGAAACAGAACAAATCGCTGCCCTCTGCCAGCAGGACTGGGTGGTCCAAGAATCGGCAAATGA 258
M S L W V K Q N N R C P L C Q Q D W V V Q R I G K * 85

C

ROC1-Hs	22	FEVKWNAVALWANDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWL---KTRQVCPLDNREWEF	108
ROC1-Dm	22	FEVKWNAVALWANDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWL---KTRQVCPLDNREYDF	108
ROC1-Ce	24	FEVKWSAVALWANDIVVDNCAICRNHIMDLCIECQANQAAGLKDECTVAWGNCNHAFHFHCISRWL---KTRQVCPLDNREWEF	110
ROC1-At	32	FEIKWSAVALWANDIVVDNCAICRNHIMDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWL---KTRQVCPLDNSEWEF	118
ROC1-Sp	21	FEIKWNAVALWQWDIVVDNCAICRNHIMDLCIECQANTDSAAQECTVAWGTCHNHFHFHCISRWL---NTRNVCPLDNREWEF	113
ROC1-Sc	35	FEIKWTAVALFWSDIADVNCAICRNHIMEPCIECQPKAMTDNECVAAWGVCNHAFHLHCKWKI---KTRDACPLDNQPWL	121
ROC2-Hs	2	FSLKWNAAVAMSWDVECDTCAICRVQVMDACLRCQAEN---KQEDCVVVWGECNHSPHNCCMSLWV---KQNNRCPLCQDWVV	85
ROC2-Ce	30	FVLKWNALAVWAWDVECDTCAICRVHLMEECLRCQSEP---SAE-CYVVGDCNHSPHHCCMTQWI---RQNNRCPLCQDWVV	112
APC11-Hs	3	VKIKCWNGVATLWVANDENCIGICRMAFNGCCPDCKVPG----DDCPLVWGQCSHCFHMHCILKWLHAQQVQQHCPMCQEWKF	84
APC11-Dm	3	VTIKSWTGVATWRVIANDENCIGICRMSFESTCPICALPG----DDCPLVWGVCNSHCFHMHCIVKWLNLQPLNKQCPMCQSWKF	85
APC11-Ce	51	ITVKKLHVCGEWKL[3]DTCGICRMEFESACNMCKEPG----DDCPLVLGICRHAFHRHIDKWI{5}QPRAQCPLCRQDWTFI	135
APC11-Sc	3	VKINEVHSVFAWSW[21]DVCGICRASYNGTCPSCKFPG----DQCPLVIGLHHNFHDHCIVRWLDPTSKGLCPMCQTFQL	165

FQKYGH"

BASE COUNT	85 a	75 c	94 g	73 t
ORIGIN				
Query Match 100.0%; Score 327; DB 9; Length 327;				
Best Local Similarity 100.0%; Pred. No. 3.6e-91;				
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	1 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGGCAAGAAG 60			
Qy	61 CGCTTGAAAGTGAAGGAAAGTGGAAATGCAGTAGGCCCTGGGATATTGTGGTTGAT 120			
Db	61 CGCTTGAAAGTGAAGGAAAGTGGAAATGCAGTAGGCCCTGGGATATTGTGGTTGAT 120			
Qy	121 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTCATAGAATGTCAGCTAACAG 180			
Db	121 AACTGTGCCATCTGCAGGAACCACATTATGGATCTTCATAGAATGTCAGCTAACAG 180			
Qy	181 GCGTCCGCTACTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAACCATGCTTTCAC 240			
Db	181 GCGTCCGCTACTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAACCATGCTTTCAC 240			
Qy	241 TTCCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300			
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Qy	301 TGGGAATTCCAAAAGTATGGGCACTAG 327			
Db	301 TGGGAATTCCAAAAGTATGGGCACTAG 327			

RESULT 2

AF140598

LOCUS AF140598- 508 bp mRNA linear PRI 11-MAY-1999
 DEFINITION Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
 ACCESSION AF140598
 VERSION AF140598.1 GI:4769003
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 508)
 AUTHORS Kamura,T., Koeppl,D.M., Conrad,M.N., Skowyra,D., Moreland,R.J.,
 Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
 Conaway,R.C., Harper,J.W. and Conaway,J.W.
 TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF
 ubiquitin ligase
 JOURNAL Science 284(5414), 657-661-(1999)
 MEDLINE 99234320
 PUBMED 10213691
 REFERENCE 2 (bases 1 to 508)
 AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma

Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA

FEATURES Location/Qualifiers
source 1. .508
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1. .508
/gene="RBX1"
CDS 7. .333
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/note="ring finger-like protein; component of VHL tumor
suppressor complex and SCF ubiquitin ligase"
/codon_start=1
/product="ring-box protein 1"
/protein_id="AAD29715.1"
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BASE COUNT 126 a 106 c 124 g 152 t

ORIGIN

Query Match 100.0%; Score 327; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 3.6e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCAGCGATGGATGTGGATACCCGAGCGGCCACCAACAGCGCGCGGGCAAGAACG 60
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Db 7 ATGGCGGCAGCGATGGATGTGGATACCCGAGCGGCCACCAACAGCGCGCGGGCAAGAACG 66

Qy 61 CGCTTTGAAGTGAAAAGTGGAAATGCAGTAGCCCTCTGGCCTGGATATTGTGGTTGAT 120
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 CGCTTTGAAGTGAAAAGTGGAAATGCAGTAGCCCTCTGGCCTGGATATTGTGGTTGAT 126

Qy 121 AACTGTGCCATTCGAGGAACCACATTATGGATCTTGCATAGAATGTCAGCTAAC 180
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 AACTGTGCCATTCGAGGAACCACATTATGGATCTTGCATAGAATGTCAGCTAAC 186

Qy 181 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGAGTCTGTAACCATGCTTTCAC 240
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATGGGAGTCTGTAACCATGCTTTCAC 246

Qy 241 TTCCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACAACAGAGAG 300
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 TTCCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACAACAGAGAG 306

Qy 301 TGGGAATTCCAAAAGTATGGGCACTAG 327
||| ||||| |||||
Db 307 TGGGAATTCCAAAAGTATGGGCACTAG 333

RESULT 3

BC001466

LOCUS BC001466 544 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, ring-box 1, clone MGC:1481 IMAGE:3138751, mRNA,
complete cds.
ACCESSION BC001466
VERSION BC001466.1 GI:12655214